

FILE 'MEDLINE, CAPLUS' ENTERED AT 07:34:19 ON 23 DEC 2003

L20 10 S PSTPIP1
L21 5 DUP REM L20 (5 DUPLICATES REMOVED)
L22 11 S CD2BP1
L23 7 DUP REM L22 (4 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 07:39:19 ON 23 DEC 2003

FILE 'MEDLINE, BIOSIS, CAPLUS, ESBIODBASE' ENTERED AT 07:39:32 ON 23 DEC 2003

L24 18 S A230T
L25 5 DUP REM L24 (13 DUPLICATES REMOVED)

=>



Single Nucleotide Polymorphism



PubMed

Nucleotide

Protein

Genome

Structure

PopSet

Taxonomy

Search

SNP



for

Go

Clear

[Limits](#)
[Preview](#)
[Index](#)
[History](#)
[Clipboard](#)
[Details](#)

SNP's linked from LocusLink

SNP's are linked from Locus PSTPIP1 via the following methods:

[Contig Annotation](#)
[GenBank\(mrna\) Mapping](#)

the list of rs# to Batch Query.

the list of rs# to file.

GENERAL

[Contact Us](#)
[dbSNP Homepage](#)
[SNP Science Primer](#)
[Announcements](#)
[dbSNP Summary](#)
[FTP SERVER](#)
[Getting Started](#)
[Build History](#)
[Handle Request](#)

DOCUMENTATION

[FAQ](#)
[Overview](#)
[How to Submit](#)
[RefSNP Summary Info](#)
[Database Schema](#)
[pdf](#)
[Changes NEW](#)
[Data Formats](#)
[Heterozygosity](#)
[Computation](#)

SEARCH

[Entrez SNP](#)
[Blast SNP](#)
[Batch Query](#)
[By Submitter](#)
[New Batches](#)
[Method](#)
[Population](#)
[Detail](#)
[Class](#)
[Publication](#)
[Chromosome Report](#)
[Locus Information](#)
[STS Markers](#)
[Free Form Search](#)
[Simple](#)
[Advanced](#)

HAPLOTYPE

[Specifications](#)
[Sample HapSet](#)
[Sample Individual](#)

Gene Model (mRNA alignment) information from genome sequence

Total gene model (contig mRNA transcript):

1




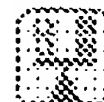





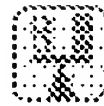



Contig	mrna	protein	mrna orientation	snp graph
NT_010194	NM_003978	NP_003969	forward	transcript




☒ in gene region
 ☐ cSNP
 ☐ has frequency
 ☐ double hit
 ☐ haplotype tagged

Contig	mrna	protein	mrna orientation
NT_010194	NM_003978	NP_003969	forward





Contig position	dbSNP rs# cluster id)	Hetero-zygosity	Validation	3D OMIM	Function	dbSNP Protein allele residue
48078109	rs2458253	N.D.			untranslated	
48078338	rs2254441	0.500			intron	
48080361	rs1022197	N.D.			intron	
48080481	rs1022198	N.D.			intron	
48080620	rs5021805	N.D.			intron	
48081180	rs7176360	N.D.			intron	
48081552	rs2469230	N.D.			intron	
48081918	rs869884	N.D.			intron	
48083121	rs2458249	N.D.			intron	
48083137	rs2458248	N.D.			intron	
48083377	rs7167993	N.D.			intron	
48086454	rs2469203	N.D.			intron	

						
48089011	rs6495230	N.D.			intron	
48089254	rs2469232	N.D.			intron	
48093585	rs7175783	N.D.			intron	
48094059	rs8030698	N.D.			intron	
48094320	rs2469207	N.D.			intron	
48095812	rs2469235	N.D.			intron	
48098230	rs4886508	N.D.			intron	
48098707	rs7173067	N.D.			intron	
48099739	rs4451915	N.D.			intron	
48100956	rs3812911	N.D.			intron	
48100966	rs3812912	N.D.			intron	
48101035	rs3812913	N.D.			intron	
48101204	rs3812914	N.D.			intron	
48102830	rs2469198	N.D.			intron	
48104351	rs8029854	N.D.			intron	
48104625	rs4362357	N.D.			intron	
48105294	rs4420499	N.D.			intron	
48105452	rs3936040	N.D.			intron	
48108227	rs1141039	N.D.			nonsynonymous A	Lys [K]
		N.D.			contig reference G	Glu [E]
48110782	rs3841234	N.D.			intron	
48110807	rs3812915	N.D.			intron	
48111243	rs1141042	N.D.			nonsynonymous T	Leu [L]
		N.D.			contig reference G	Arg [R]
48111248	rs1141043	N.D.			nonsynonymous T	Ser [S]
		N.D.			contig reference G	Ala [A]
48111262	rs1141044	N.D.			nonsynonymous T	Asp [D]
		N.D.			contig reference G	Glu [E]
48111265	rs1141045	N.D.			nonsynonymous C	His [H]

	N.D.		contig reference	G	Gln [Q]
48112349	rs3935339	N.D.		intron	
48112856	rs2469236	N.D.		intron	
48113329	rs2469237	N.D.		intron	
48113980	rs3812916	N.D.		intron	
48115200	rs4078354	N.D.		intron	
48117741	rs6495232	N.D.		intron	

Variations in genomic region of [PSTPIP1](#)

Contig Accession	Contig position	dbSNP cluster id	rs#	Heterozygosity	Validation	3D OMIM	Function	dbSNP Pr allele	re
NT_010194	48077013	rs2469229		N.D.			locus		
NT_010194	48077189	rs2458254		N.D.			locus		

Details of GenBank mapping

Accession class	Nucleotide accession	Nucleotide Position	Hit orientation	dbSNP rs # (cluster id)	Protein accession	Function
NCBI RefSeq	NM_003978.2	236	minus strand	rs2458253	NP_003969.2	unclassified
		505	plus strand	rs1141038	NP_003969.2	unclassified
		677	plus strand	rs1141039	NP_003969.2	unclassified
		790	plus strand	rs1141040	NP_003969.2	unclassified
		799	plus strand	rs1141041	NP_003969.2	unclassified
		807	plus strand	rs1141042	NP_003969.2	unclassified
		812	plus strand	rs1141043	NP_003969.2	unclassified
		826	plus strand	rs1141044	NP_003969.2	unclassified
		829	plus strand	rs1141045	NP_003969.2	unclassified
GenBank mRNA	AF038602.1	144	plus strand	rs1141038	AAD11958.1	unclassified
		316	plus strand	rs1141039	AAD11958.1	unclassified
		429	plus strand	rs1141040	AAD11958.1	unclassified
		438	plus strand	rs1141041	AAD11958.1	unclassified
		446	plus strand	rs1141042	AAD11958.1	unclassified
		451	plus strand	rs1141043	AAD11958.1	unclassified
		465	plus strand	rs1141044	AAD11958.1	unclassified
		468	plus strand	rs1141045	AAD11958.1	unclassified
	AF038603.1	144	plus strand	rs1141038	AAD11959.1	unclassified
		316	plus strand	rs1141039	AAD11959.1	unclassified
		429	plus strand	rs1141040	AAD11959.1	unclassified
		438	plus strand	rs1141041	AAD11959.1	unclassified
		446	plus strand	rs1141042	AAD11959.1	unclassified
		451	plus strand	rs1141043	AAD11959.1	unclassified

	465	plus strand	rs1141044	AAD11959.1	unclassified
	468	plus strand	rs1141045	AAD11959.1	unclassified
BC008602.1	236	minus strand	rs2458253	AAH08602.1	unclassified
	505	plus strand	rs1141038	AAH08602.1	unclassified
	677	plus strand	rs1141039	AAH08602.1	unclassified
	790	plus strand	rs1141040	AAH08602.1	unclassified
	799	plus strand	rs1141041	AAH08602.1	unclassified
	807	plus strand	rs1141042	AAH08602.1	unclassified
	812	plus strand	rs1141043	AAH08602.1	unclassified
	826	plus strand	rs1141044	AAH08602.1	unclassified
	829	plus strand	rs1141045	AAH08602.1	unclassified
U94778.1	360	plus strand	rs1141038	AAD00762.1	unclassified
	532	plus strand	rs1141039	AAD00762.1	unclassified
	645	plus strand	rs1141040	AAD00762.1	unclassified
	654	plus strand	rs1141041	AAD00762.1	unclassified
	662	plus strand	rs1141042	AAD00762.1	unclassified
	667	plus strand	rs1141043	AAD00762.1	unclassified
	681	plus strand	rs1141044	AAD00762.1	unclassified
	684	plus strand	rs1141045	AAD00762.1	unclassified

GENERAL: [Contact Us](#) | [Homepage](#) | [Announcements](#) | [dbSNP Summary](#) | [Genome](#) | [FTP SERVER](#) | [Build History](#) | [Handle Request](#)

DOCUMENTATION: [FAQ](#) | [Overview](#) | [How to Submit](#) | [RefSNP Summary](#) | [Info](#) | [Database Schema](#)

SEARCH: [Entrez SNP](#) | [Blast SNP](#) | [Main Search](#) | [Batch Query](#) | [By Submitter](#) | [New Batches](#) | [Method](#) | [Population](#) | [Publication](#) | [Chromosome Report](#) | [Batch](#) | [Locus Info](#) | [Free Form](#) | [Easy Form](#) | [Between Marker](#)

HAPLOTYPE: [Specifications](#) | [Sample HapSet](#) | [Sample Individual](#)

NCBI: [PubMed](#) | [Entrez](#) | [BLAST](#) | [OMIM](#) | [Taxonomy](#) | [Structure](#)

[Disclaimer](#) [Privacy statement](#)

Revised August 11, 2003 2:18 PM